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Contribution of the Long Arm of Chromosome 10 to the Total Heterosis Observed in Five Maize Hybrids

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Abstract
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Disciplines
Agricultural Science | Agronomy and Crop Sciences | Genetics and Genomics | Plant Breeding and Genetics

Comments

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Contribution of the Long Arm of Chromosome 10 to the Total Heterosis Observed in Five Maize Hybrids

K. R. Lamkey,* A. R. Hallauer, and D. S. Robertson

ABSTRACT

Knowledge of the contributions of different chromosome segments to the expression of quantitative traits is limited. Information on the relative importance of loci on different chromosome arms could be used to identify blocks of genes that might be useful for improving inbreds and their hybrid progeny. One suggested technique to evaluate the relative importance of different chromosome arms of maize (Zea mays L.) for trait expression has been the use of B-A translocations. The objective of our study was to measure the contributions of the 10L segments from the inbreds B55, CI187-2, Oh43, M14, and N25 to the total heterotic effect observed in the hybrid of W22 and the respective inbreds. Field studies were conducted that included three strains of W22, their crosses to B55, CI187-2, Oh43, N25, and M14; and their crosses to five W22 lines that carried a substitution from each of the five non-W22 lines for the distal 67% of the long arm of chromosome 10 (1OL). Data were collected for 11 plant and ear traits. Significant differences (P ≤ 0.05) were detected among the three strains of W22 and their crosses. The differences, however, did not show a consistent pattern among strains for the 11 traits. Significant midparent heterosis was detected for most traits in the hybrids of the normal and 10L segment lines for grain yield and components of yield. The percentage of midparent heterosis accounted for by the 10L segment ranged from 9.4 to 20.8% for yield. There were differences among traits for the effects of segment 10L on trait expression, with the greatest effect for tassel-branch number and the least for kernel weight. These studies suggest that the use of B-A translocations to analyze more chromosome segments may be informative and may make possible the combining of different segments for creating superior lines and hybrids.

Robertson et al. (1981) presented the results of the first test of a technique using B-A translocations to transfer intact chromosome segments from one inbred line of maize to another (Robertson, 1964; 1967; Peterson and Wernsman, 1964). The technique involved transferring intact, the distal 67% of the long arm of chromosome 10 (10L) from four inbreds (i.e., B55, Oh43, CI187-2, and M14) into the inbred W22 background. Robertson et al. (1981) measured the effects of these chromosome 10L segments from different inbreds on performance as measured by 11 quantitative traits. In no instance did the substituted lines per se perform better than W22. Hybrids between different substituted lines were homozygous for most of the W22 genome, but heterozygous for the distal 67% of the long arm of chromosome 10 (e.g., B55, 10L/M14, Oh43 10L/CI187-2 10L, etc.). Many of these hybrids performed better than W22 for some traits, but in no case did the hybrids exceed the best substituted parent line. Heterotic responses of the hybrids of the four substituted lines with the inbred W22 were observed in nine instances.

In the study reported by Robertson et al. (1981), the substituted lines were compared to and hybridized with W22(IA). They indicated that the use of W22(IA) complicated the interpretation of their results and could have biased the conclusions because two different strains of W22 were involved. The substituted lines have the background of W22 R-scm2, although they were crossed to W22(IA) to determine the effects of the 10L substituted segment.

We evaluated three strains of W22 per se [W22(IA), W22 R-scm2, and W22(WI)], in crosses with five normal, and five 10L substituted lines, and in crosses with


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The experiment was grown at the Iowa State Agronomy Farm and overplanted and thinned to 18 plants per row (44,023 plants were collected on the center row of each plot. All plots were 6 m long with 0.76 m between rows, were used to eliminate block design with three replications. Three row plots, 5.38 m long, were used to distinguish them from the substituted lines), W22 strains, and the indicated inbred homozygous strains.

The stocks used in this study included:

- W22 (a W22 strain obtained from Jerry Kermicle, maintained at the University of Wisconsin and obtained from Donald S. Robertson at Iowa State University, W22(IA), an inbred line maintained by self pollination, W22(WI), a stock of W22, and a purple aleurone W22 line obtained from Jerry Kermicle, and the three strains of W22; and (iii) measure the contribution of the 10L segments from the inbreds B55, CI187-2, Oh43, M14, and N25 to the total heterotic effect observed in the hybrid of W22 and the respective normal lines.

The procedures for generating the substituted W22 hybrids were as follows:

- The 46 entries were evaluated in a randomized complete-block design with three replications.
- The results of the 1981 experiments were repeatable; the effects of the treatments were significant across experiments (years).

The objectives of our study were to:

1. Determine if there were genetic differences among the three strains of W22; and
2. Measure the contributions of the 10L segments from the inbreds B55, CI187-2, Oh43, M14, and N25 to the total heterotic effect observed in the hybrid of W22 and the respective normal lines.

The 1981 experiments were conducted with three replications, each consisting of three rows, 5.38 m long, 0.76 m between rows, and 18 plants per row. The effects of the treatments were significant across experiments (years). All effects in the model were considered fixed except years and replications. The LSD at the 0.05 level was 0.74 for 1 yr. The LSD for comparing means in the same row was based on the mean square from the row analysis of variance.

The means for yield and other agronomic traits are summarized in Table 1. The environmental conditions were excellent for maize production in 1982 and 1984, and average in 1983. The mean grain yields were 4.83, 3.57, and 4.57 Mg ha⁻¹, respectively, for normal lines, 10L substituted line, and W22 strain crosses. The heterosis in the corresponding normal line × W22 hybrid and the MP hybrid was calculated as 100 times the ratio of the MP heterosis in the 10L substituted line × W22 hybrid to the MP heterosis in the W22 strain hybrid. The standard error of MP heterosis was calculated as the square root of the mean square error of MP heterosis divided by the number of replications. The LSD at the 0.05 level was 0.74.
<table>
<thead>
<tr>
<th>Genotype</th>
<th>Ear length</th>
<th>Cob diameter</th>
<th>Kernel depth</th>
<th>Days to silk</th>
<th>Tassel branches</th>
<th>Seed weight R-scm²</th>
<th>Seed yield</th>
<th>Coefficient of variation</th>
</tr>
</thead>
<tbody>
<tr>
<td>W22(IA) x OH43</td>
<td>7.06</td>
<td>15.8</td>
<td>17.8</td>
<td>4.5</td>
<td>2.7</td>
<td>0.88</td>
<td>13.6</td>
<td>292.3</td>
</tr>
<tr>
<td>W22(IA) x N25</td>
<td>7.16</td>
<td>16.5</td>
<td>20.0</td>
<td>4.7</td>
<td>3.0</td>
<td>0.86</td>
<td>17.0</td>
<td>301.7</td>
</tr>
<tr>
<td>W22(IA) x M14</td>
<td>6.79</td>
<td>18.0</td>
<td>20.7</td>
<td>4.5</td>
<td>2.8</td>
<td>0.83</td>
<td>13.2</td>
<td>241.0</td>
</tr>
<tr>
<td>W22(IA) x CI187-2</td>
<td>7.89</td>
<td>16.7</td>
<td>21.2</td>
<td>4.6</td>
<td>2.9</td>
<td>0.83</td>
<td>13.6</td>
<td>284.3</td>
</tr>
<tr>
<td>W22(IA) x B55</td>
<td>8.62</td>
<td>16.4</td>
<td>19.3</td>
<td>4.3</td>
<td>2.9</td>
<td>0.73</td>
<td>19.2</td>
<td>302.0</td>
</tr>
</tbody>
</table>

Comparison of W22 Inbred Strains

There were significant differences (P < 0.05) among the strains of W22, although W22(WI) was usually significantly different compared with either W22(IA) or W22

Perhaps the best method of evaluating differences among strains of W22 for quantitative traits is to compare the midparent (MP) heterosis observed in the three possible crosses among the W22 strains. MP heterosis was not dependent on the normal or 10L substituted lines. Differences among the means of W22 strains averaged over hybrids with the 10L substituted lines was not significant for any of the traits except kernel weight, indicating that the performance of the W22 strains was more alike genotypically than from either W22(WI) or W22
### Table 1: Heterosis Values and Standard Errors

<table>
<thead>
<tr>
<th>Trait</th>
<th>Normal 10L</th>
<th>Substituted Lines</th>
<th>10L Substituted</th>
<th>W22 R-sere2</th>
<th>R-scm2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to Silking</td>
<td>15.2</td>
<td>15.5</td>
<td>16.1</td>
<td>15.2</td>
<td>15.4</td>
</tr>
<tr>
<td>Ear Length</td>
<td>22.5</td>
<td>23.0</td>
<td>23.5</td>
<td>22.7</td>
<td>22.4</td>
</tr>
<tr>
<td>Kernel-Row Number</td>
<td>10.4</td>
<td>10.8</td>
<td>11.0</td>
<td>10.5</td>
<td>10.3</td>
</tr>
<tr>
<td>Kernel Size</td>
<td>4.2</td>
<td>4.3</td>
<td>4.4</td>
<td>4.1</td>
<td>4.2</td>
</tr>
<tr>
<td>Ear Diameter</td>
<td>1.8</td>
<td>1.9</td>
<td>2.0</td>
<td>1.8</td>
<td>1.9</td>
</tr>
<tr>
<td>Cob Diameter</td>
<td>5.7</td>
<td>5.8</td>
<td>6.0</td>
<td>5.7</td>
<td>5.9</td>
</tr>
<tr>
<td>Plant Height</td>
<td>10.5</td>
<td>10.7</td>
<td>11.0</td>
<td>10.6</td>
<td>10.7</td>
</tr>
<tr>
<td>Ear to Silk Distance</td>
<td>4.5</td>
<td>4.7</td>
<td>4.8</td>
<td>4.6</td>
<td>4.7</td>
</tr>
</tbody>
</table>

Significant at the 0.05 and 0.01 probability levels, respectively.

- Standard error of the mean over the five lines for each of the W22 strains.
- Mean 0.77** 0.6** 1.0* 0.1 0.1* 0.04 10* 6** - 1.1 3.5** - 0.5
- W22(WI) × W22: 0.92** 0.8* 0.9 0.1 0.1* 0.06 16 6 -1.5 2.5* 8.3
- Genotype yield rows length Ear Cob depth Plant Ear to silk branches weight
- Table ing than CI187-2 10L and N25 10L.
- The W22 carry alleles detrimental to line per se performance in scm2, by comparing the performance of the 10L substituted counterparts (Table 1). The effect of the substituted Oh43 10L, which were equal in yield to their normal and Russell, 1968; and Busch and Russell, 1964).
- The changes observed in W22(IA) seemingly were due to either W22(IA) or W22(WI) × W22 having accumulated unfavorable alleles during maintenance. These results were not entirely unexpected. All of the 10L substituted lines were lower yielding than the W22 strains per se. Hybrid W22(IA) × W22(IA) was significantly higher yielding than all the W22 strains, while the hybrid W22(IA) × W22(WI) was not significantly different from either of the other two hybrids or from the W22(WI). The results for the other traits were similar to the results for yield.
Table 4. Percentage of total midparent heterosis observed in the normal line x W22

<table>
<thead>
<tr>
<th>Genotype yield</th>
<th>rows</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
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<tr>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

Results from our study suggest that much of the heterosis observed in the 10L substituted lines x W22(WI) crosses may be due to the heterosis observed in the 10L substituted lines × R-scm2. Crosses of the 10L substituted lines to W22(IA) were contributed earlier flowering to hybrids with W22(IA). The MP heterosis values of crosses to the normal line x W22(WI) per se. All traits of the 10L substituted lines were in the background of W22 R-scrrt2. Perhaps the best way of comparing the effects of the 10L segments across different strains is using the MP heterosis values, which are based on crosses to the normal line. This method helps in understanding the genetic alterations in strains of inbred lines. Busch and Russell (1964) discuss how tester lines may mask masking effects of crossing to the normal lines. This, however, cannot be interpreted as evidence that W22(IA) is genetically similar to the other two W22 strains because of the early flowering in hybrids with W22(IA). The MP heterosis values for the W22(R-scm2) hybrid had significantly more kernel rows than W22(R-scm2) per se and significantly inferior to W22(R-scm2) per se. The Oh43 10L segment contributed to significantly higher kernel weight. In no instance did a 10L substituted line × W22(WI) hybrid have a significantly higher yielding hybrid than W22(WI) per se. The M14 10L segment produced a significantly higher yielding hybrid than the N25 10L segment contributed to significantly longer ears and the B55 10L segment contributed earlier flowering to hybrids with W22(IA). The heterotic effect of the 10L substituted lines is carrying dominant genes for increased tassel number. Other than the M14 10L line for kernel weight, significant MP heterosis for grain yield was observed for crosses of B55 10L, CI187-2 10L, N25 10L, and Oh43 10L to W22(R-scm2). A comparison of the relative size of the heterotic effects for the different segments. The MP heterosis values for the W22(R-scm2) × B55 10L, W22(R-scm2) × CI187-2 10L, W22(R-scm2) × N25 10L, and W22(R-scm2) × Oh43 10L are not significant in the normal line x W22(R-scm2) hybrids. Use of MP heterosis values allows two important comparisons to be made: (i) a comparison of the relative size of the heterotic effects for many of the yield component traits. We do not consider the overall lack of heterotic effects for many of the same yield component traits. We generally, the four hybrids with significant heterotic effects for the M14 10L × W22(R-scm2), B55 10L, CI187-2, and Oh43 10L to W22(R-scm2) served for crosses of B55 10L, CI187-2 10L, N25 10L, and Oh43 10L to W22(R-scm2). The heterotic effect of the 10L substituted lines cannot be attributed solely to the substituted chromosome segment. In crosses with W22(WI), only the B55 10L segment served for crosses of B55 10L, CI187-2 10L, N25 10L, and Oh43 10L to W22(WI). Robertson et al. (1981) emphasized that consideration of the overall lack of heterotic effects for many of these traits is controlled by loci with alleles in the additive to partial dominance range (Hallauer and Miranda, 1981).
The absence of a heterotic effect does not preclude the possibility that a particular segment carries either favorable or unfavorable alleles for a trait; it requires directional dominance (Falconer, 1981). If the genes on the 10L chromosome segment were in the partial dominance range, one could not prove whether the substituted segment was allelically identical to W22 R-scm2. There were significant heterotic effects for ear length, ear diameter, and tassel-branch number. The heterotic effects for cob diameter were significant for four of the five substituted lines, but they were too small to be of practical importance. Significant heterotic effects for the M14 10L X W22 R-scm2 hybrid were significant for kernel-row number, although definite conclusions cannot be drawn for the other traits. The possibility of additive gene action for some segment were additive, then a significant heterotic effect would not be expected. Additive gene action requires directional dominance (Falconer, 1981). If the substituted segment could only be demonstrated that the segment has an effect on tassel-branch number, it would be allelically identical to W22 R-scm2. There were significant heterotic effects for ear length, ear diameter, and tassel-branch number. The heterotic effects for CI187-2 10L per se. In contrast, M14 10L per se exhibited a large positive effect for tassel-branch number, but an effect on tassel-branch number was unexpected because there was no related effect observed for CI187-2 10L X W22 R-scm2. The percentage of total MP heterosis attributed to the genome was contributing to the heterotic effects for ear length, ear diameter, and tassel-branch number. The comparison of M14 10L hybrids were not observed for the plant and ear traits. The results reported here establish the feasibility of future to begin to combine different regions with a unique genotype, these factors are expected to result in the variable results observed.

For those situations where the substituted segments were not expected or were difficult to detect from such small segments of the genome. Because each hybrid has different combinations of chromosome segments, certain combinations of segments in hybrid combinations. Such studies could be used to identify blocks of genes that might be useful for improving inbreds and their hybrid progeny. As more segments are analyzed it may be possible in the future to begin to combine different regions with a unique genotype, these factors are expected to result in the variable results observed.

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